Microbiome studies generally focus on the gut microbiome, which is composed of a large proportion of commensal bacteria. Here we propose a first analysis of the liver microbiome using next generation sequencing as a tool to detect potentially pathogenic strains. We used *Peromyscus leucopus*, the main reservoir host species of Lyme disease in eastern North America, as a model and sequenced V5-V6 regions of the 16S gene from 18 populations in southern Quebec (Canada). The *Lactobacillus* genus was found to dominate the liver microbiome. We also detected a large proportion of individuals infected by *Bartonella vinsonii arupensis*, a human pathogenic bacteria responsible for endocarditis, as well as *Borrelia burgdorferi*, the pathogen responsible for Lyme disease in North America. We then compared the microbiomes among two *P. leucopus* genetic clusters occurring on either side of the St. Lawrence River, and did not detect any effect of the host genotype on their liver microbiome assemblage. Finally, we report, for the first time, the presence of *B. burgdorferi* in a small mammal host from the northern side of the St. Lawrence River, in support of models that have predicted the northern spread of Lyme disease in Canada.

Keywords: 16S, NGS, *Peromyscus leucopus*, Microbiome, *Borrelia*, *Bartonella*

P3. Characterization of the rice microbiota: development and contribution of the 'culturomics' approach.

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Plant microbiota that colonizes different compartments of the plant host plays a key-role in nutrient availability, growth promotion and plant health. Understanding and managing plant microbiota could allow promoting beneficial microbial communities and reducing the impacts of detrimental microbes. While metabarcoding analyses targeting different regions of the 16S rRNA have recently gained popularity to describe large microbial communities of different ecosystems, these culture-independent surveys may have presented a depth bias and failed in detecting microbial populations with low concentrations. The diversification of culture conditions together with a high throughput identification by mass spectrometry system (MALDI-TOF), i.e. a culturomics approach, can greatly increase the number of detected species (Lagier et al., 2015). Microbial culturomics has been shown to reveal new bacterial repertoires non covered by metabarcoding sequencing in the human gut microbiome study (Lagier et al., 2015). In some cases, culture techniques detected even more bacterial species. In addition, a better understanding of the ecology of the plant-associated microbiota and the interactions between members of the community may require the use of synthetic microbial communities. Using rice as a plant model we aim at describing the spatio-temporal dynamics of rice endophyte microbiota. The 16S rRNA metabarcoding approach will be combined with culturomics approaches in order to compare both molecular and 'cultivable' diversity and evaluate their potential complementarity. Our objectives are to (i) establish a culture collection, (ii) develop a MALDI-TOF database for routine identification of bacterial isolates and (iii) compare the metabarcoding approach and the culturomics approach in terms of characterization of microbial community diversity. We isolated more than 2000 bacterial colonies from superficially rice disinfected tissues collected in two rice fields of Camargue in the Provence region of France. Colonies were first identified by a sanger sequencing of the complete 16S rRNA gene. These colonies were also identified by mass spectrometry and the score identification obtained from the current MALDI-TOF database revealed gaps in identifying plant-associated bacteria. One challenge will be to enrich the database with data from plants to make it valuable in plant microbiota analyses. We will further compare the community diversity as described by the metabarcoding approach and the 'cultivable'

fraction.

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Keywords: Mass spectrometry, Endophytes

P4. Genomic insights into the pathogenicity of *Rickettsiella* spp., intracellular bacteria of arthropods.

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Gammaproteobacteria of the genus *Rickettsiella*, closely related to *Legionella* and *Coxiella*, are well known as pathogenic bacteria in many arthropods (Bouchon et al. 2011). In woodlice, while *Rickettsiella* was primarily only described as a virulent agent (Bouchon et al., 2011; Cordaux et al., 2007), we showed that some strains may be non-pathogenic (Dittmer et al., 2016; Bouchon et al. 2016). Non-pathogenic strains were also reported in aphids where they act as mutualists conferring benefits to their hosts by protecting against predators (Tsuchida et al. 2010) or a fungal pathogen (Lukasik et al. 2012). *Rickettsiella* was recently found highly abundant in ticks with no evidence of virulence (Duron et al. 2016). However, a strain initially identified as *Diplorickettsia massiliensis* (Mediannikow et al. 2010) but nested in the *Rickettsiella* genus (Leclerque & Kleespies 2012), was later recognized as a human pathogen (Subramanian et al. 2012). *Rickettsiella* therefore constitutes a particularly interesting group to study the evolutionary emergence of pathogenicity. Unfortunately, there are only a very few genomic data for *Rickettsiella*: only one whole and annotated genome of *R. isopodorum* from the woodlouse *Trachelipus rathkei* has been recently published (Wang & Chandler 2016), whereas two draft genomes were available: *R. grylli* isolated from an unidentified woodlouse (GenBank AAQJ00000000) and *D. massiliensis* from the tick *Ixodes ricinus* (Mathew et al. 2012). Interestingly several genomic islands have been identified in *R. isopodorum* but absent in *R. grylli*. By NGS metagenomics approaches, we completed these data with five new genomes of *Rickettsiella* from distinct species of woodlice. Phylogenomics showed that these genomes were closely related to *R. grylli* and *R. isopodorum* but distantly related from *D. massiliensis*, all belonging to a well-defined *Rickettsiella* genus. Comparative genomics allowed us to identify T4SS secretion systems and a high number of putative virulence factors including eukaryote-like domain-containing proteins.

Keywords: Pathogenicity, *Rickettsiella*, Intracellular, Bacteria, Arthropods

P5. Host-pathogen-commensal interactions in fish.

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